WHAT IS CLAIMED IS:

1. An isolated polypeptide comprising the amino acid sequences selected from the group consisting of SEQ ID NOs: 2, 4 and 6, and fragments thereof.

2. The isolated polypeptide of Claim 1, wherein the fragments comprise the amino acid residues 60 to 69 of SEQ ID NO: 2.

3. The isolated polypeptide of Claim 1, wherein the fragments comprise the amino acid residues 67 to 76 or 72 to 98 of SEQ ID NO: 4.

4. The isolated polypeptide of Claim 1, wherein the fragments comprise the amino acid residues 451 to 460 or 455 to 472 of SEQ ID NO: 6.

5. An isolated nucleic acid comprising the nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3 and 5, and fragments thereof.

6. The isolated nucleic acid of Claim 5, wherein the fragments comprise nucleotides 253 to 258 of SEQ ID NO: 1.

7. The isolated nucleic acid of Claim 5, wherein the fragments comprise nucleotides 273 to 278 of SEQ ID NO: 3.

8. The isolated nucleic acid of Claim 5, wherein the fragments comprise nucleotides 1424 to 1429 of SEQ ID NO: 5.

9. An expression vector comprising the nucleic acid of Claim 5.

10. A host cell transformed with the expression vector of Claim 9.

11. A method for producing the polypeptide of Claim 1, which comprises the steps of:

(1) culturing the host cell of Claim 10 under a condition suitable

for the expression of the polypeptide; and

(2) recovering the polypeptide from the host cell culture.

12. An antibody specifically binding to the polypeptide of Claim 1.

13. A method for diagnosing the diseases associated with the deficiency of the SGII gene in a mammal, in particular cancers, which comprises detecting the nucleic acid of Claim 5 or the polypeptide of Claim 1.

14. The method of Claim 13, wherein the detection of the nucleic acid of Claim 5 comprises the steps of:

(1) extracting total RNA from a sample obtained from the mammal;

(2) amplifying the RNA by reverse transcriptase-polymerase chain reaction (RT-PCR) to obtain a cDNA sample;

(3) bringing the cDNA sample into contact with the nucleic acid of Claim 5; and

(4) detecting whether the cDNA sample hybridizes with the nucleic acid of Claim 5.

15. The method of Claim 14 further comprising the step of determining the amount of the hybridized sample.

16. The method of Claim 13, wherein the detection of the nucleic acid of Claim 5 comprises the steps of:

(1) extracting the total RNAs of cells obtained from the mammal;

(2) amplifying the RNA by reverse transcriptase-polymerase

chain reaction (RT-PCR) with a set of primers to obtain a cDNA comprising the fragments comprising nucleotides 253 to 258 of SEQ ID NO: 1 or nucleotides 273 to 278 of SEQ ID NO: 3 or nucleotides 1424 to 1429 of SEQ ID NO: 5; and

(3) detecting whether the cDNA is obtained.

17. The method of Claim 13, wherein the detection of the nucleic acid of Claim 5 comprises the steps of:

(1) extracting the total RNAs of cells obtained from the mammal;

(2) amplifying the RNA by reverse transcriptase-polymerase chain reaction (RT-PCR) with a set of primers to obtain a cDNA comprising the fragments comprising nucleotides 240 to 269 of SEQ ID NO: 1 or nucleotides 261 to 290 of SEQ ID NO: 3 or nucleotides 1413 to 1442 of SEQ ID NO: 5; and

(3) detecting whether the cDNA is obtained.

18. The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides 253 to 258 of SEQ ID NO: 1 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 at any other locations downstream of nucleotide 258, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 containing nucleotides 253 to 258 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 1 at any other locations upstream of nucleotide 253.

19. The method of Claim 17, wherein the forward primer has a sequence comprising the nucleotides 240 to 269 of SEQ ID NO: 1 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 at any other locations downstream of nucleotide 269, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 containing nucleotides 240 to 269 and the

forward primer has a sequence comprising the nucleotides of SEQ ID NO: 1 at any other locations upstream of nucleotide 240.

20. The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides 273 to 278 of SEQ ID NO: 3 and the reverse primer has a sequence complementary to the sequence complementary to the nucleotides of SEQ ID NO: 3 at any other locations downstream of nucleotide 278, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 3 containing nucleotides 273 to 278 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 3 at any other locations upstream of nucleotide 273.

21. The method of Claim 17, wherein the forward primer has a sequence comprising the nucleotides 261 to 290 of SEQ ID NO: 3 and the reverse primer has a sequence complementary to the sequence complementary to the nucleotides of SEQ ID NO: 3 at any other locations downstream of nucleotide 290, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 3 containing nucleotides 261 to 290 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 3 at any other locations upstream of nucleotide 261.

22. The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides 1424 to 1429 of SEQ ID NO: 5 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 5 at any other locations downstream of nucleotide 1429, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 5 containing nucleotides 1424 to 1429 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 5 at any other locations upstream of nucleotide 1424.

23. The method of Claim 17, wherein the forward primer has a sequence comprising the nucleotides 1413 to 1442 of SEQ ID NO: 5 and

the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 5 at any other locations downstream of nucleotide 1442, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 5 containing nucleotides 1413 to 1442 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 5 at any other locations upstream of nucleotide 1413.

24. The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 1 at any other locations upstream of nucleotide 253 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 at any other locations downstream of nucleotide 258.

25. The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 3 at any other locations upstream of nucleotide 273 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 3 at any other locations downstream of nucleotide 278.

26. The method of Claim 16, wherein the forward primer has a sequence the nucleotides of SEQ ID NO: 5 at any other locations upstream of nucleotide 1424 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 5 at any other locations downstream of nucleotide 1429.

27. The method of Claim 24, the cDNA sample amplified from SEQ ID NO: 1 is 339bp shorter than that from SGII.

28. The method of Claim 25, the cDNA sample amplified from SEQ ID NO: 3 is 259bp shorter than that from SGII.

29. The method of Claim 26, the cDNA sample amplified from SEQ ID NO: 5 is 533bp shorter than that from SGII.

30. The method of Claim 16 further comprising the step of

detecting the amount of the amplified cDNA sample.

31. The method of Claim 13, wherein the detection of the polypeptide of Claim 1 comprises the steps of contacting the antibody of Claim 12 with protein samples extracted from the mammal, and detecting whether an antibody-polypeptide complex is formed.

32. The method of Claim 31 further comprising the step of determining the amount of the antibody-polypeptide complex.